

**BLASTN 2.2.8 [Jan-05-2004]**Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1079572591-7810-120835507754.BLASTQ3

Query=

(1115 letters)

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)

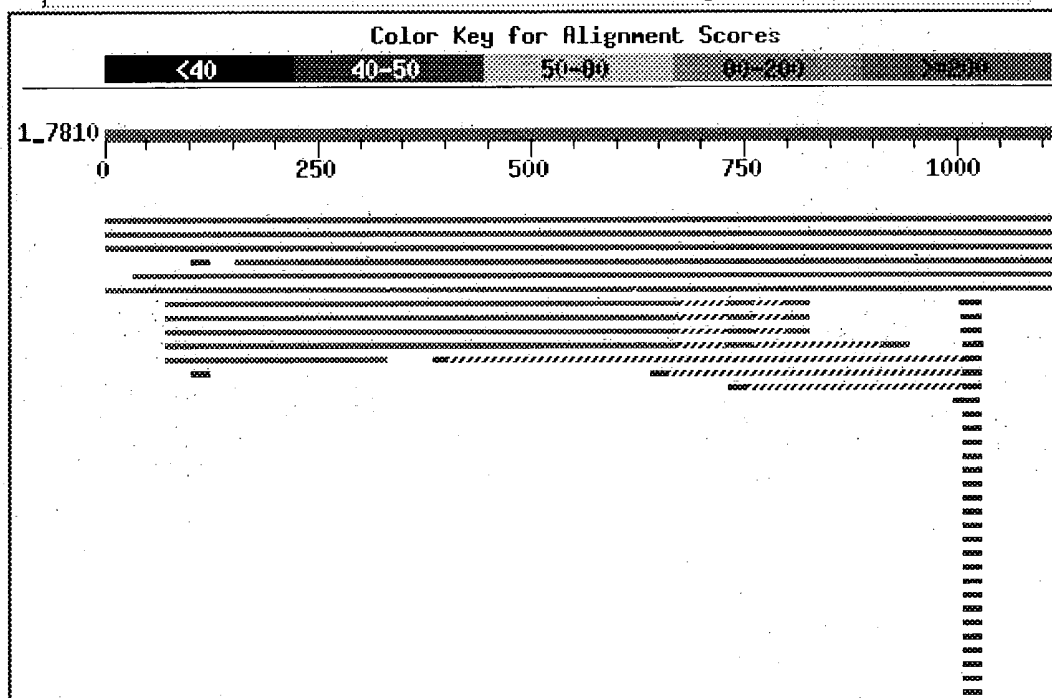
2,102,977 sequences; 10,130,642,339 total letters














If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 168 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments



Sequences producing significant alignments:			Score (bits)	E Value	
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gi 39930574 ref NM_198149.1 	Homo sapiens chromosome 1 open...	1805	0.0		2004
gi 16306970 gb BC009558.1 	Homo sapiens chromosome 1 open r...	1797	0.0		2004
gi 38541262 gb BC061908.1 	Homo sapiens chromosome 1 open r...	1467	0.0		2004
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gi 16973029 emb AL513217.11 	Human DNA sequence from clone ...	734	0.0		40% 15 Nov 2001
gi 26333272 dbj AK039457.1 	Mus musculus adult male spinal ...	613	e-172		2003
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gi 31982176 ref NM_175259.3 	Mus musculus RIKEN cDNA 933013...	605	e-170		
gi 34880245 ref XM_341125.1 	Rattus norvegicus similar to s...	581	e-162		
gi 12860937 dbj AK020369.1 	Mus musculus adult male diencep...	219	9e-54		
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Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|37182299|gb|AY358589.1|



Homo sapiens clone DNA59842 PPAG583 (UNQ583) mRNA

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Identities = 1091/1141 (95%), Gaps = 26/1141 (2%)
Strand = Plus / Plus

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
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 Strand = Plus / Plus

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Query: 940 ttc--wtagtccctctgctccc-mgatcccagccagg-mggctggggccctactgtttgt 995
||| |||||
Sbjct: 965 ttcaaatagtccctctgctcccaagatcccagccaggaaggctggggccctactgtttgt 1024

Query: 996 cccctctgggctggggtggggggaggaggaggttccgtcagcagctggcagtagccctc 1055
|||||
Sbjct: 1025 cccctctgggctggggtggggggaggaggaggttccgtcagcagctggcagtagccctc 1084

Query: 1056 ctctctggctgccccactggccacatctctggcctgctagatt-aagctgtaaagacara 1114
|||||
Sbjct: 1085 ctctctggctgccccactggccacatctctggcctgctagattaaagctgtaaagacaaa 1144

Query: 1115 a 1115
|
Sbjct: 1145 a 1145

```

 >gi|38541262|gb|BC061908.1|  Homo sapiens chromosome 1 open reading frame 40, m
IMAGE:4415188), partial cds
Length = 1000

Score = 1497 bits (745), Expect = 0.0
Identities = 935/984 (95%), Gaps = 25/984 (2%)
Strand = Plus / Plus

```

Query: 154 gctcccctggtgctggccggcgaggactgcctgtggtacctggaccggm-tggctcctgg 212
|||||
Sbjct: 1 gctcccctggtgctggccggcgaggactgcctgtggtacctggaccggaatggctcctgg 60

Query: 213 catccggggtttm-ctgcgagttcttcaccttctgctgcgggacctgctaccatcggtac 271
|||||
Sbjct: 61 catccggggtttaactgcgagttcttcaccttctgctgcgggacctgctaccatcggtac 120

Query: 272 tgctgcagggacctgaccttgcttatcaccgagaggcagcagm-gcactgcctggccttc 330
|||||
Sbjct: 121 tgctgcagggacctgaccttgcttatcaccgagaggcagcagaagcactgcctggccttc 180

Query: 331 agcccm-gaccatagcaggcatcgccctcagctgtgatcctctttgttgctgtggttgcc 389
|||||
Sbjct: 181 agcccaagaccatagcaggcatcgccctcagctgtgatcctctttgttgctgtggttgcc 240

Query: 390 accaccatctgctgcttcctctgttcctgttgctacctgtaccgccggcgccagcagctc 449
|||||
Sbjct: 241 accaccatctgctgcttcctctgttcctgttgctacctgtaccgccggcgccagcagctc 300

Query: 450 cagagcccatTTG-mggccaggagattcc-mtgacaggcatcccagtgcagccagtatac 507

```



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|||||
Sbjct: 301 cagagcccatttgaaggccaggagattccaatgacaggcatcccagtgacagccagtatac 360

Query: 508 ccataccccaggacccc--wgctggccctgcacccccacagcctggcttcatgtacca 565
|||||
Sbjct: 361 ccataccccaggacccc aaagctggccctgcacccccacagcctggcttcatataacca 420

Query: 566 cctagtggctcctgctcccc-mtatccactctaccagctgggccccagctctac-mccct 623
|||||
Sbjct: 421 cctagtggctcctgctccccaatatccactctaccagctgggccccagctctacaacct 480

Query: 624 gcagctcctcctccctatatatgccaccacagccctcttaccgggagcct--gggmccagc 681
|||||
Sbjct: 481 gcagctcctcctccctatatatgccaccacagccctcttaccgggagcctgaggaaccagc 540

Query: 682 catgtctctgctgcccccttcagtgatgcc-mccttgggagatgcctcatcctgtacctg 740
|||||
Sbjct: 541 catgtctctgctgcccccttcagtgatgccaaccttgggagatgcctcatcctgtacctg 600

Query: 741 catctggctcctgggggtggcaggagtcctccagccaccaggccccagacc-mgcc-mgcc 798
|||||
Sbjct: 601 catctggctcctgggggtggcaggagtcctccagccaccaggccccagaccaagccaagcc 660

Query: 799 ctgggccctactggggacagagccccagg-gmgtgg-mcaggagctg-mctagaactatg 855
|||||
Sbjct: 661 ctgggccctactggggacagagccccagggaagtggaacaggagctgaactagaactatg 720

Query: 856 aggggttgggggagggccttgg-mttatgggctatttttactgggggc-mgggagggaga 913
|||||
Sbjct: 721 aggggttgggggagggccttgggaattatgggctatttttactgggggcaagggagggaga 780

Query: 914 tgacagcctgggtcacagtgcctgttttc--wtagtcctctgctccc-mgatcccagcc 970
|||||
Sbjct: 781 tgacagcctgggtcacagtgcctgttttcaaatagtcctctgctcccaagatcccagcc 840

Query: 971 agg-mggctggggccctactgtttgtcccctctgggctgggggtgggggagggaggaggt 1029
|||
Sbjct: 841 aggaaggctggggccctactgtttgtcccctctgggctgggggtgggggagggaggaggt 900

Query: 1030 tccgtcagcagctggcagtagccctcctctctggctgccccactggccacatctctggcc 1089
|||||
Sbjct: 901 tccgtcagcagctggcagtagccctcctctctggctgccccactgaccacatctctggcc 960

Query: 1090 tgctagatt-aagctgtaaagaca 1112
|||||
Sbjct: 961 tgctagattaaagctgtaaagaca 984
```